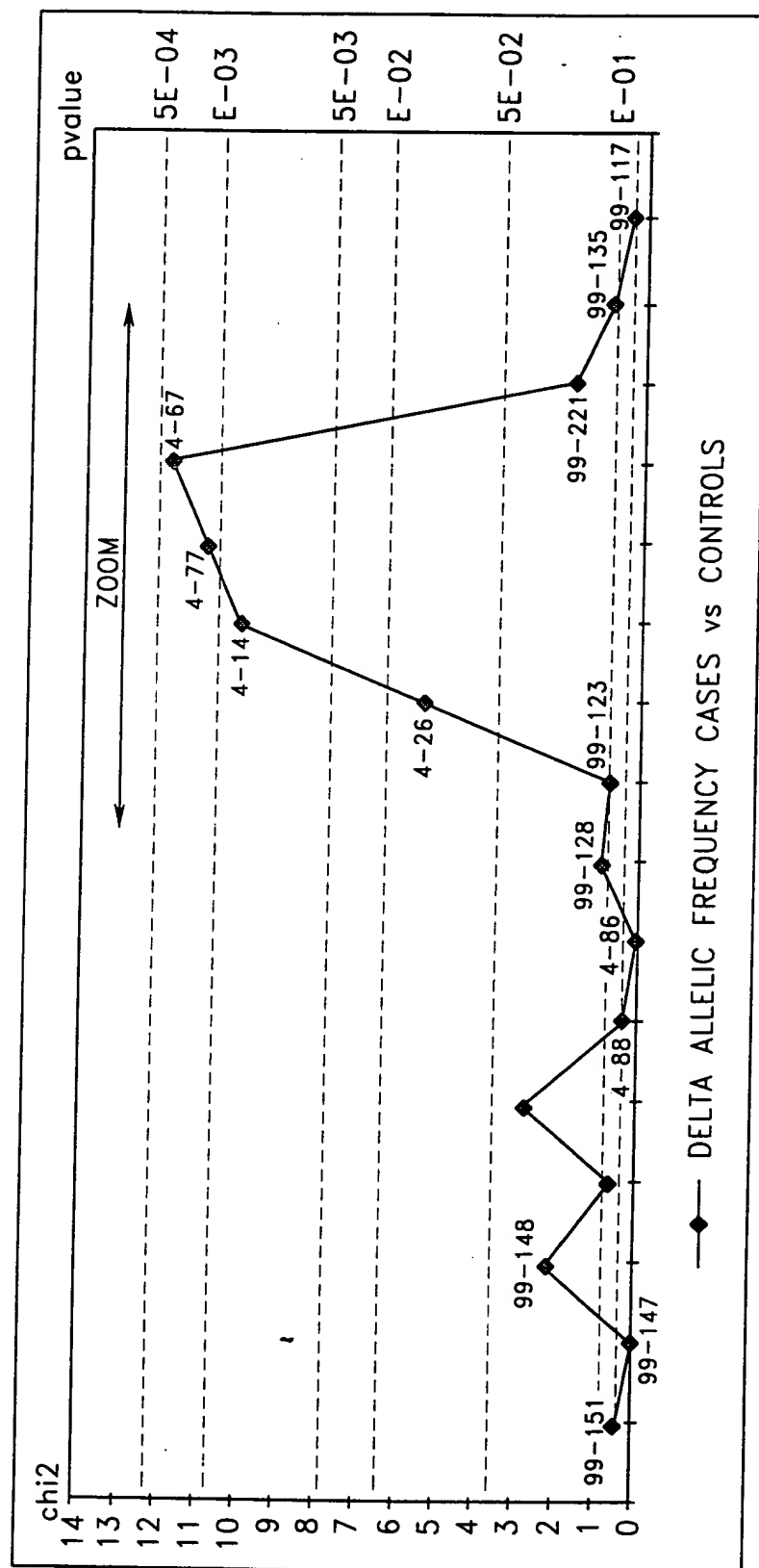


FIG. 1

POPULATION SAMPLE SIZE	AFFECTED CASES= 112	NON AFFECTED CONTROLS=76
POPULATION CHARACTERISTICS	35 SPORADIC CASES +77 FAMILIAL CASES	>65 YEARS PSA <4



**FIG. 2**

# ASSOCIATION STUDIES (ZOOM)

CHARACTERISTICS OF POPULATIONS	AFFECTED CASES (185)	UNAFFECTED CONTROLS (104)
	47 SPORADIC CASES +138 FAMILIAL CASES	>65 YEARS PSA<4

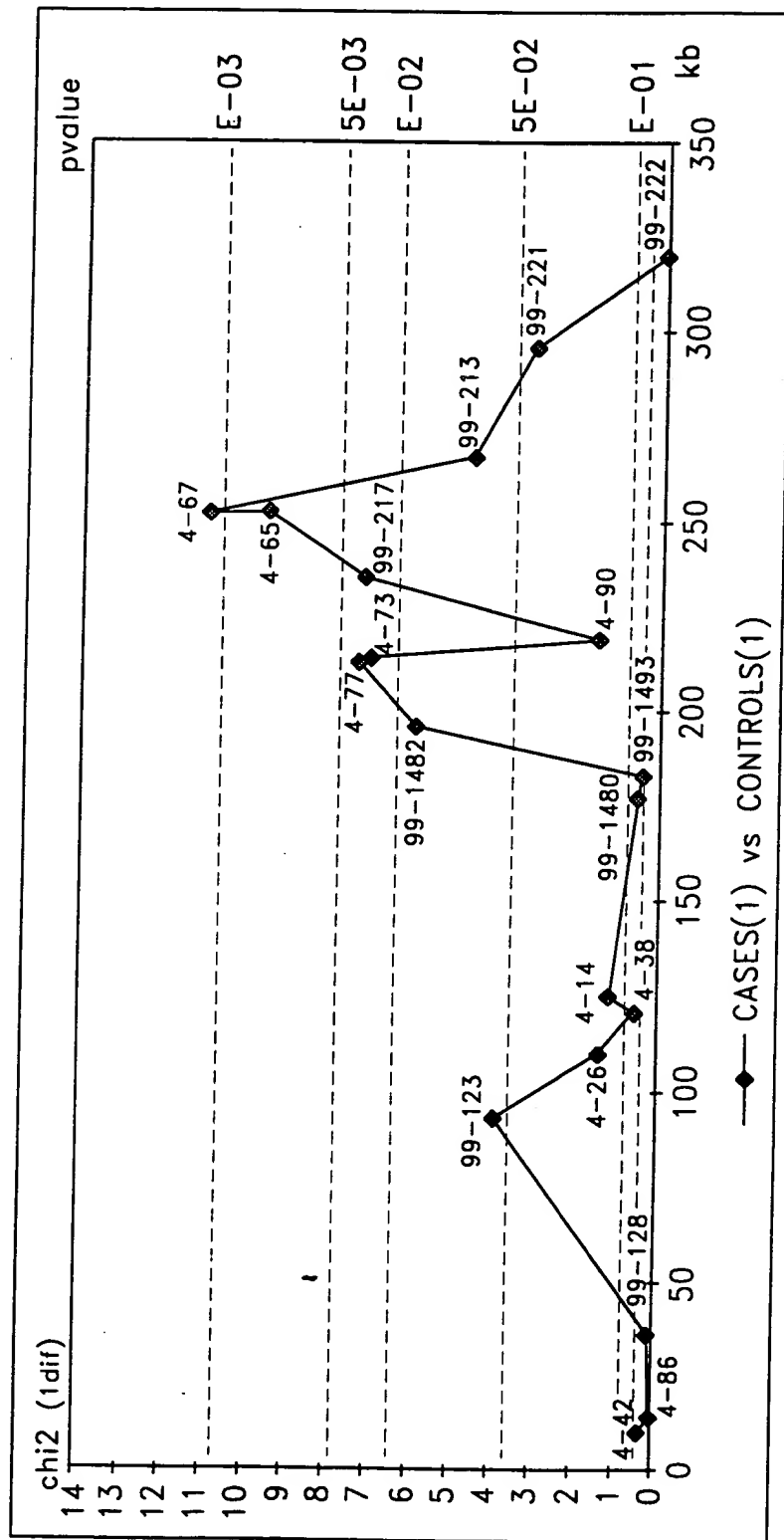


FIG.3

## HAPLOTYPE FREQUENCY ANALYSIS

	AFFECTED	UNAFFECTED
	CASES 2 (281)	CONTROLS 3 (130)
CHARACTERISTICS OF POPULATIONS	143 SPORADIC CASES +138 FAMILIAL CASES	>65 YEARS PSA <4

MARKERS	99-123	4-26	4-14	4-77	99-217	4-67	99-213	99-221	99-135
BACS	H0287B09	B0189E08				B0463F01			B0725B12
CONTIGS									
GENES									
				11453					
				← PG1 →					
P VALUE	2,00E-01 <sub>t</sub> *	1,00E-01*	2,00E-02**	2,00E-02**	2,00E-025,00E-04***	9,00E-02*	7,00E-02*	12,00E-04*	
DISTANCE BETWEEN MARKERS(KB)	<18KB>	<15KB>	<88KB>	<22KB>	<17KB>	<15KB>	<29KB>	>>100KB<	
HAPLOTYPE 8>304KB<	C	A	C	G	T	G	A	A	
HAPLOTYPE 7>286KB<		A	C	G	T	G	A	A	
HAPLOTYPE 6<186KB>		A	C	G	T	G	A		
HAPLOTYPE 5<171KB>			C	G	T	G	A		
HAPLOTYPE 4<83KB>				G	T	G	A		
HAPLOTYPE 3.1<54KB>					T	G	A		
HAPLOTYPE 3.2<54KB>				G	T	G			
HAPLOTYPE 2.2<39KB>				G	T				
HAPLOTYPE 2<32KB>					T	G			
HAPLOTYPE 1.1<17KB>					T				
HAPLOTYPE 1.2<15KB>						T	G		

**FIG. 4**

# HAPLOTYPE SIMULATIONS (100 ITERATIONS)

MARKERS	4-144-7799-2174-67				99-21399-221	HAPLOTYPE FREQUENCIES		RELATIV RISK	PVALUE	
	C		G			CASES	CONTROLS			
HAPLOTYPE							0,117	0,013	10,06	9,00E-07

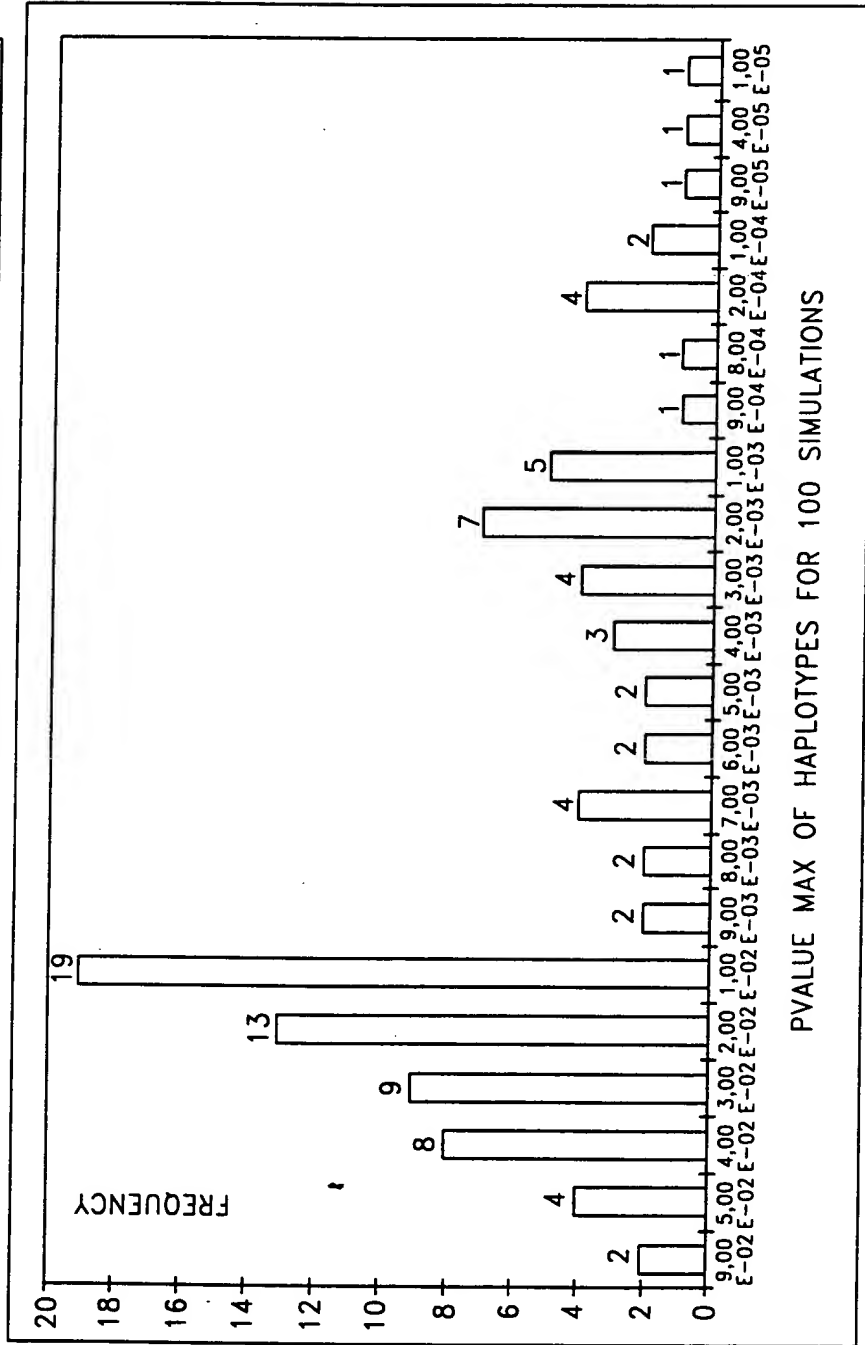


FIG.5A



BAC	MARKER	SEQ ID N°	SEQ ID N°(MUT)	PU SEQUENCE	SEQ ID N°	RP SEQUENCE	SEQ ID N°	POLYMORPHISM POSITION*	BASE	MICROSEQ. OLIGOS POSITIONS*
228	99-123	21	30	AAAGCCAGGACTAGAAGG	39	TATCAGAAAGGAGTGGG	48	24	C/T	1-23 25-47 (COMPLEMENTARY)
189	4-26	22	31	TACAGCCCTGTAAGACAC	40	TGAGGACTGCTAGGAAG	49	24	A/G	1-23 25-47 (COMPLEMENTARY)
228/189	4-14	23	32	TCTAACCTCTCATCCAAC	41	GACTGTATCTTTGATGCAC	50	24	C/T	1-23 25-47 (COMPLEMENTARY)
189/463	4-77	24	33	TGTGATTTACAGCGGCG	42	GGAAAGGTACTCATCATAG	51	24	G/C	1-23 25-47 (COMPLEMENTARY)
463	99-217	25	34	GGTGGGAATTTACTATATG	43	GTTTATTTTGTGTGAGCTTTG	52	24	C/T	1-23 25-47 (COMPLEMENTARY)
189/463	4-67	26	35	AAGTCCACCTTCTCAAGC	44	TGAAAGAGTTTATGCTCTGG	53	24	C/T	1-23 25-47 (COMPLEMENTARY)
463	99-213	27	36	ATACTGGCAGCGGTGCTTC	45	TTATTGCCCCACACATGCTTGAG	54	24	C/T	1-23 25-47 (COMPLEMENTARY)
463	99-221	28	37	CCCTTTTCTTCACTGCTC	46	TCATTCGTCTGGCTAGGTC	55	24	A/C	1-23 25-47 (COMPLEMENTARY)
725	99-135	29	38	TGGAAGTGTATTGCCCC	47	AAACACCTCTCCCATTTGTC	56	24	A/G	1-23 25-47 (COMPLEMENTARY)

FIG. 6A

\*: POSITIONS ARE GIVEN RELATIVE TO THE SEQUENCE OF THE CORRESPONDING MARKER (i.e. SEQ ID N° 21-38 AND 57-62)

BAC	MARKER	SEQ ID N°	SEQ ID N°(MUT)	PU SEQUENCE	SEQ ID N°	RP SEQUENCE	SEQ ID N°	POLYMORPHISM POSITION*	BASE	MICROSEQ. OLIGOS POSITIONS*
189/463	99-1482	57	60	ATCAAATCAGTGAAGTCTGAG	63	ACAAATCTATATAAGGCTGG	66	24	A/C	1-23 25-47 (COMPLEMENTARY)
463	4-73	58	61	ATCGCTGGAACATTTCTGG	64	CTCTTGTTAAACACGAGTG	67	24	G/C	1-23 25-47 (COMPLEMENTARY)
463	4-65	59	62	GATTTAAGCTACGCTATTAG	65	TGGCTGCTCAATTTCTCC	68	24	C/T	1-23 25-47 (COMPLEMENTARY)

FIG. 6B

\*: POSITIONS ARE GIVEN RELATIVE TO THE SEQUENCE OF THE CORRESPONDING MARKER (i.e. SEQ ID N° 21-38 AND 57-62)





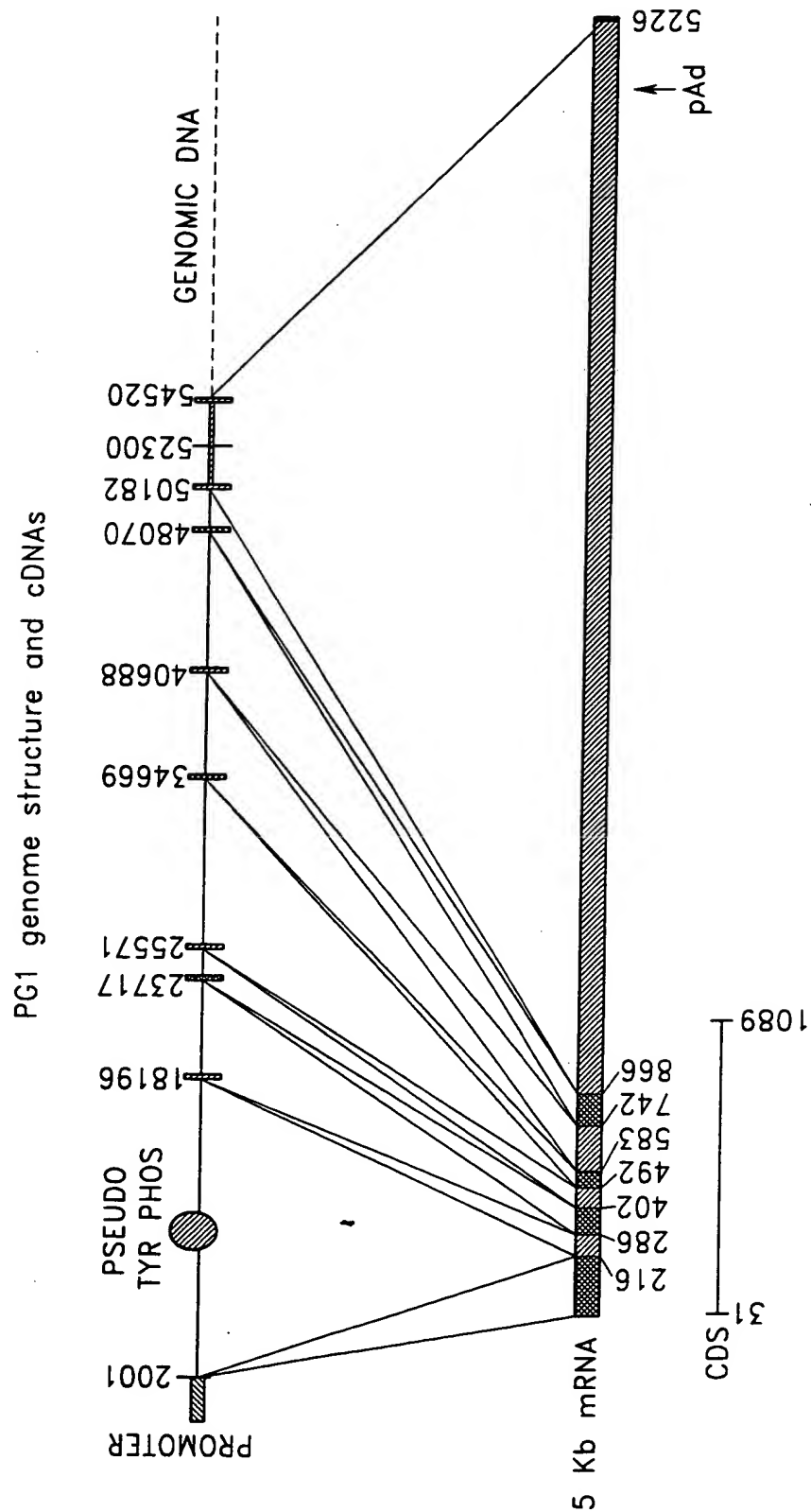
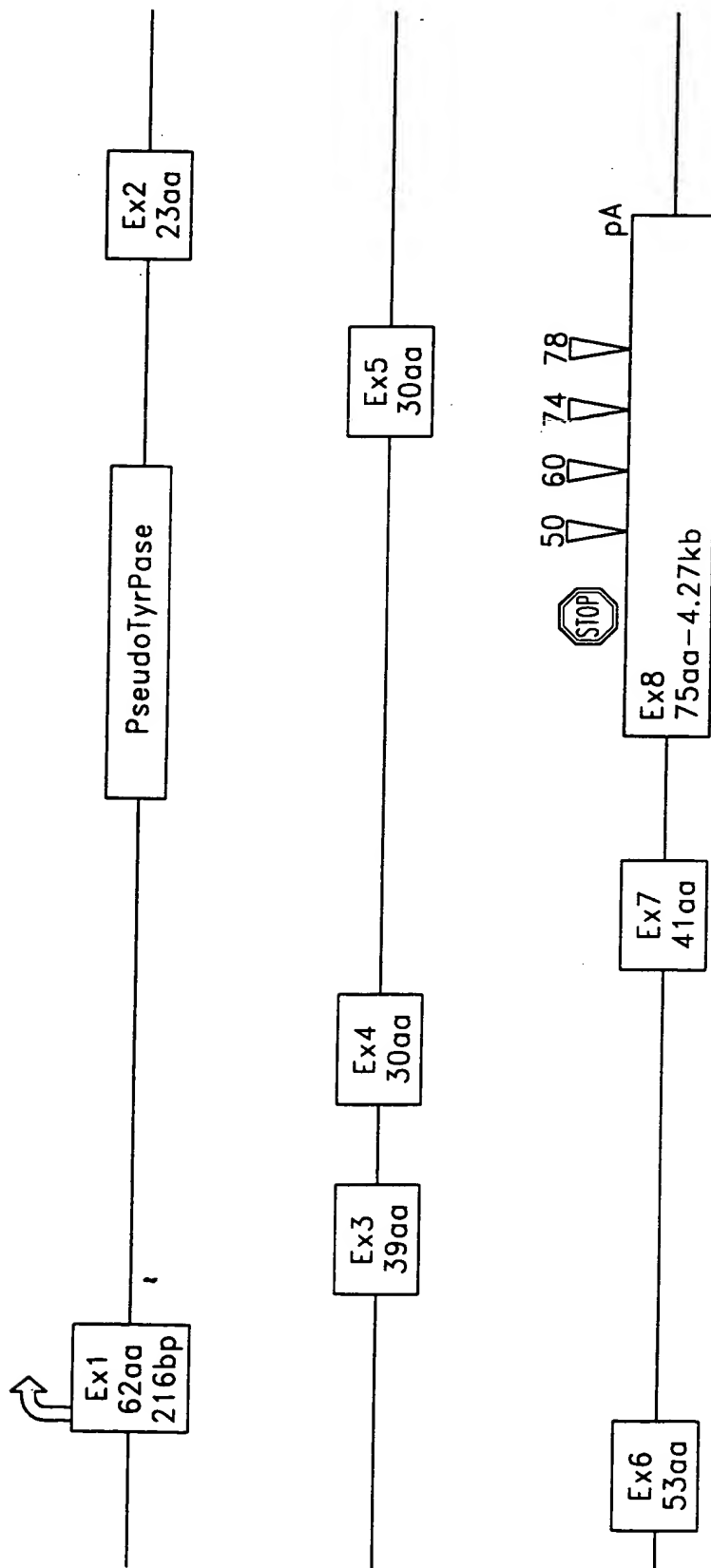


FIG.8

Prostate Gene 1

FIG. 8B



		box 1	box 2	box 3
PG1	Hs	NHQ 81-83	FPEGTR 160-165	LDAIYDVTV 211-219
AF003136 (Genbank)	Ce	NHQ 630-632	FPEGTR 712-717	LDAIYDVTV 762-770
Z72511 (Genbank)	Ce	48 NHR 50	FPEGTD 129-134	VEYIYDITI 204-212
P38226 (Swissport)	Sc	111 NHQ 113	FPEGTN 223-228	IESLYDITI 271-279
P33333 (Swissport)	Sc	81 NHQ 83	FPEGTR 154-159	-
Z49770 (Genbank)	Sc	116 NHQ 118	FPEGTN 215-220	LDAIYDVTI 265-273
P26647 (Swissport)	Ec	72 NHQ 74	FPEGTR 145-150	-
Z49860 (Genbank)	Bn	-	FVEGTR 90-95	VPAIYDMTV 138-146
U89336 (Genbank)	Hs	95 NHQ 97	FPEGTR 168-173	-
U56417 (Genbank)	Hs	103 NHQ 105	FPEGTR 176-181	-
AB005623 (Genbank)	Mm	100 NHQ 102	FPEGTR 173-178	
Z29518 (Genbank)	Zm	91 NHR 93	FVEGTR 170-175	VPAIYDTTV 218-226

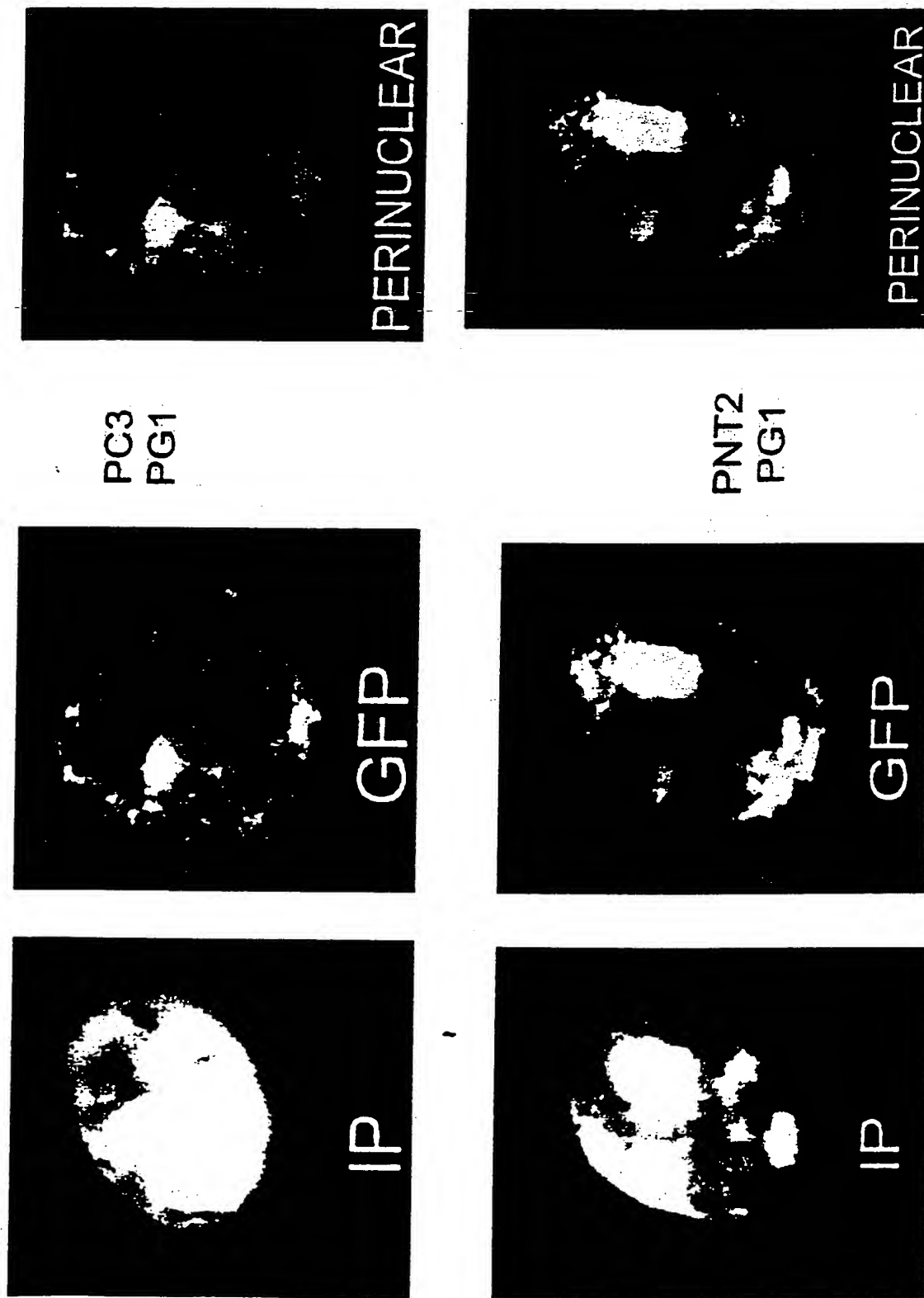
Hs = Homo sapiens, Ce = Caenorabibitis elegans, Ec = Escherichia coli;  
 Sc = Saccharomyces cerevisiae, Bn = Brassica napus, Zm = Zea maize,  
 Mm = Mus Musculus

- = pattern absent from protein sequence

Note: Functional acyl glycerol transferases all contain boxes 1 and 2 and not box 3. Proteins most related to PG1 contain the 3 boxes with a high degree of conservation.

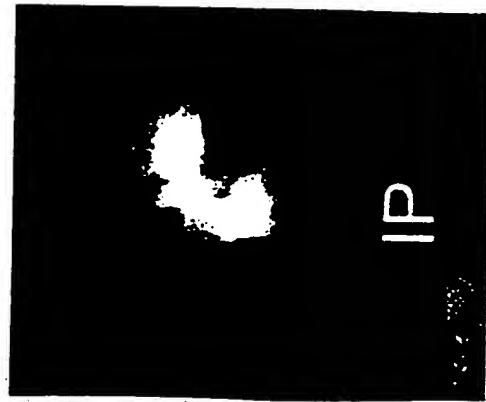
**FIG. 9**

TOP SECRET



**FIG. 10**

TOP SECRET



IP



GFP

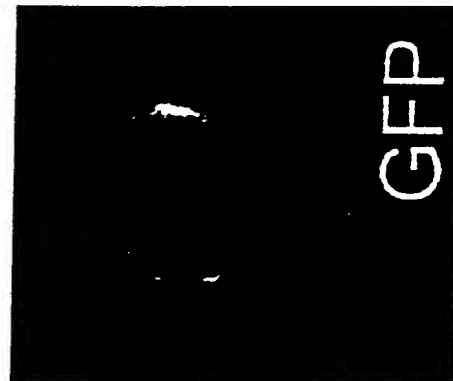
PC3  
PG1  
1-4



PERINUCLEAR



IP



GFP

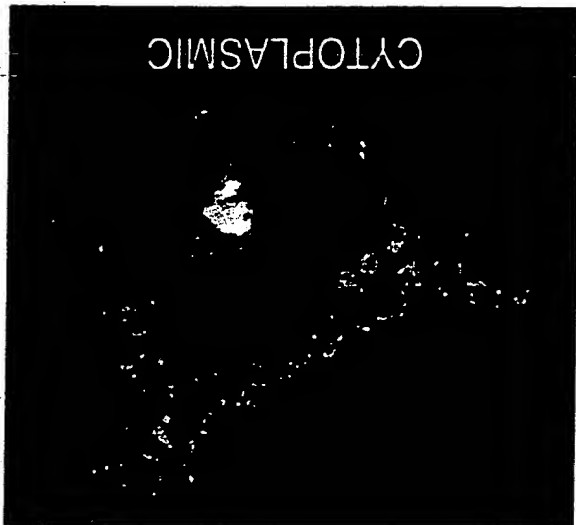
PNT2  
PG1  
1-4



PERINUCLEAR

**FIG. 11**

\_\_\_\_\_



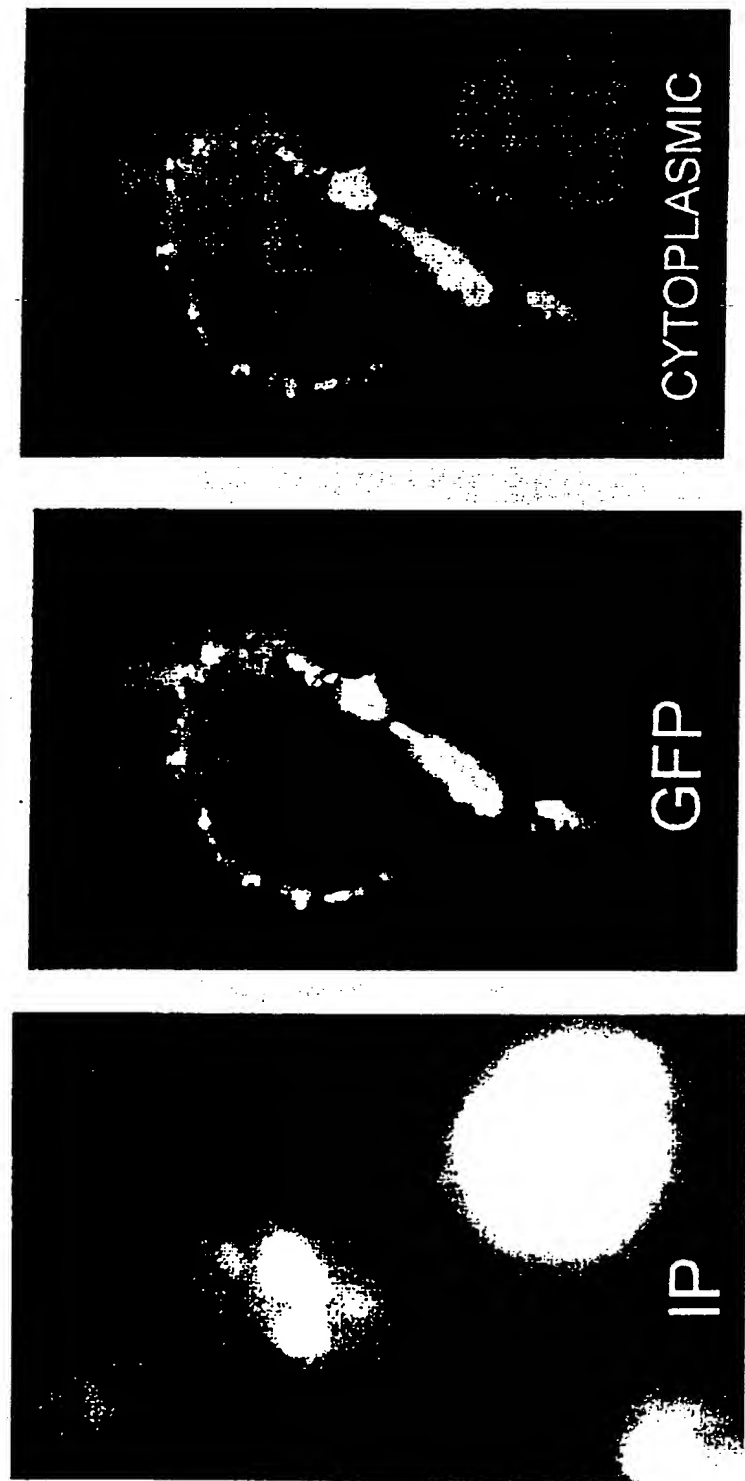
PNT2 PG1 1-5



PC3  
PG1  
1-5

[illegible]

TOP SECRET



PNT2 PG1 mut229

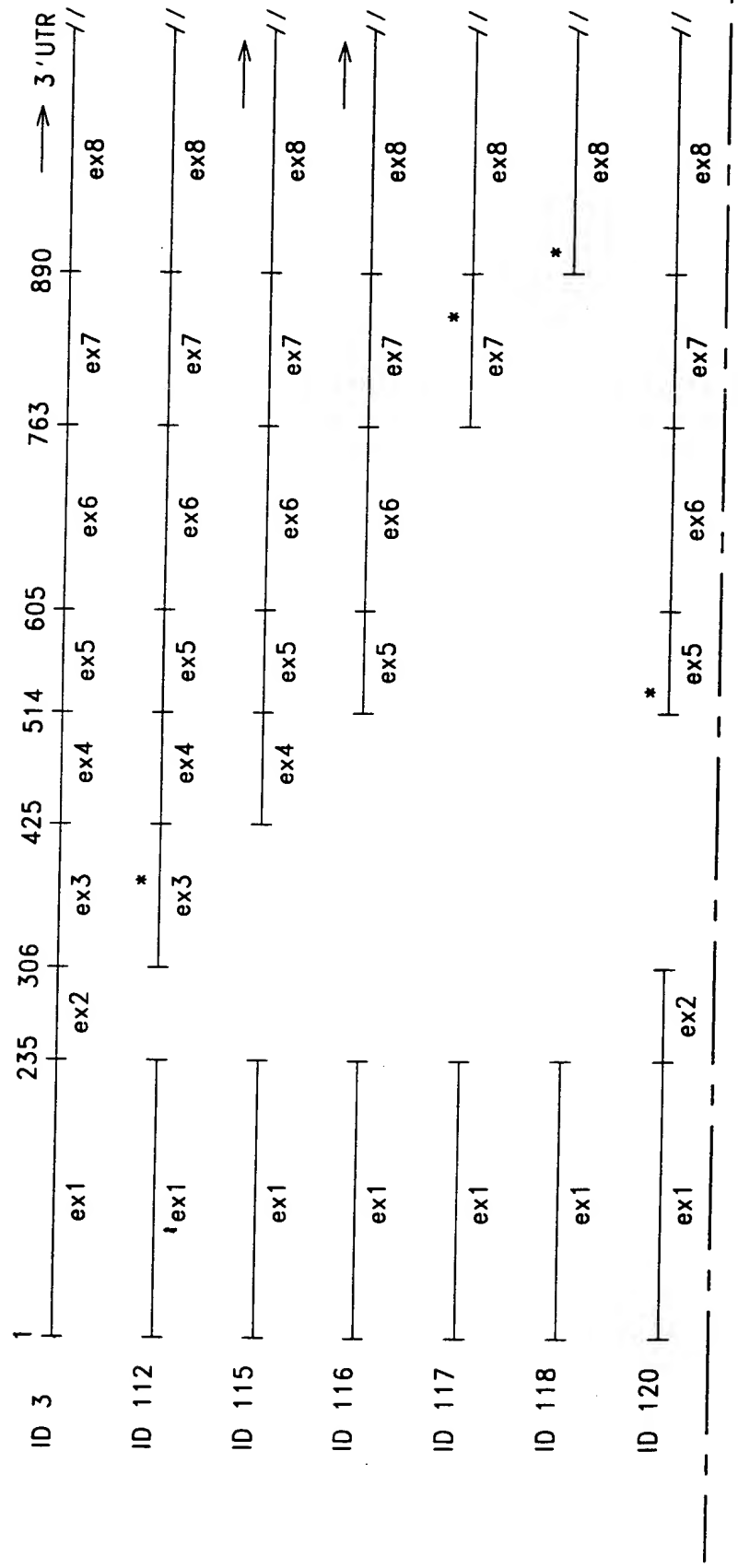
**FIG. 13**

FIG. 14A
FIG. 14B

FIG. 14

FIG. 14A

Alternative splicing





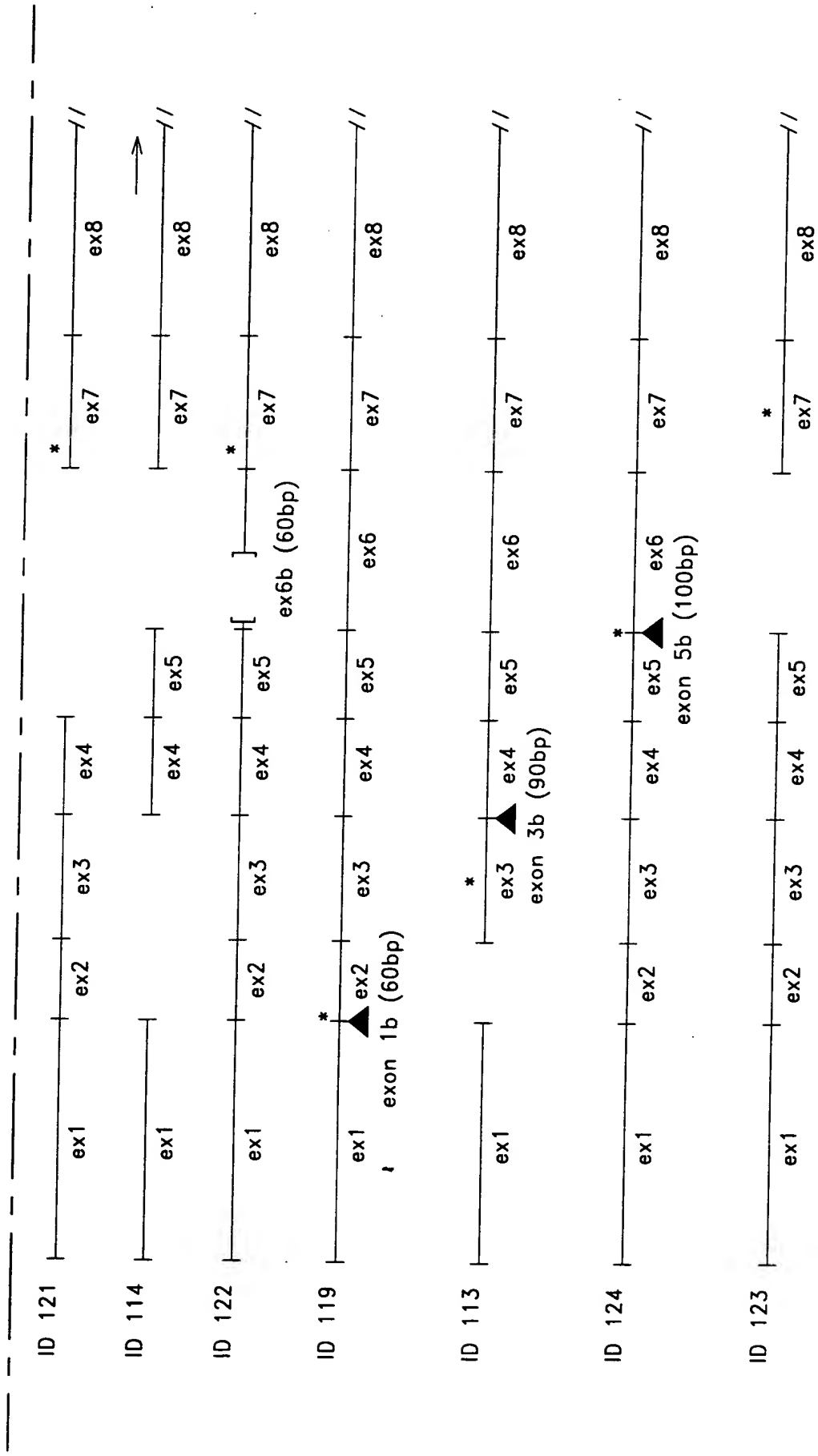


FIG. 14B

Combination of exons of PG1 gene discovered  
by PCR with primers specific for exon borders

Printer	Clones	prostate	PNT1A	PNT1B	PNT2	LnCaPFCG	LNCaPJMB	CoHPV	Du145	PC3	ECP5	ECP6	ECP7	ECP8	ECP9	ECP10	ECP11	ECP12	ECP13	ECP14	ECP15	ECP16	ECP17	ECP18	ECP19	ECP20	ECP21	ECP22	ECP23	ECP24
PG1exon13	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon14	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon15	+	-	-	-	-	-	-	NT	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PG1exon16	-	+	-	+	+	-	-	NT	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
PG1exon17	+	+	+	+	+	+	+	NT	+	+	-	-	+	-	-	-	+	+	+	+	+	+	+	+	-	-	+	+	-	+
PG1exon18	+	+	+	+	+	-	-	NT	+	+	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-
PG1exon24	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon25	+	+	-	+	+	-	-	NT	+	-	-	-	-	-	-	-	+	-	-	-	+	-	-	-	-	-	-	-	+	+
PG1exon26	+	+	+	+	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon27	-	-	-	+	+	-	-	NT	+	-	-	-	-	-	-	-	-	+	-	-	+	-	-	-	-	-	-	-	+	+
PG1exon28	-	-	+	-	-	-	-	NT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PG1exon35	-	+	+	+	+	+	+	NT	+	+	-	-	-	-	-	-	+	+	-	+	+	+	-	-	+	+	+	+	-	-
PG1exon36	+	+	+	+	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon37	-	-	-	-	-	-	-	NT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PG1exon38	-	-	-	-	-	-	-	NT	-	+	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	+	-	-	-
PG1exon46	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon47	+	+	+	+	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon48	-	-	-	-	+	-	-	NT	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PG1exon57	+	+	+	+	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon58	-	-	-	-	-	+	+	NT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
PG1exon68	-	+	+	-	+	+	+	NT	+	+	-	-	-	-	+	+	-	+	+	-	+	-	+	-	-	-	+	-	+	+
PG1exon11b	+	+	+	+	+	+	+	NT	+	+	-	+	-	+	+	+	+	+	+	+	-	-	+	-	-	+	+	+	-	+
PG1exon1b2	+	+	+	+	+	+	+	NT	+	+	-	+	-	+	+	+	+	+	+	+	-	-	+	-	-	+	+	+	-	+
PG1exon1b3	+	+	+	+	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon1b4	+	-	+	+	+	+	+	+	+	+	-	-	+	-	+	+	-	-	-	+	+	+	+	-	+	+	-	-	+	-
PG1exon1b5	+	-	+	+	+	+	+	NT	+	+	-	-	+	-	-	+	+	-	+	+	-	+	-	-	+	+	+	+	+	-
PG1exon1b6	+	+	+	+	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon1b7	+	-	+	+	+	+	+	NT	+	+	+	+	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PG1exon1b8	-	-	+	-	+	-	-	NT	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PG1exon3b4	+	+	+	+	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon3b5	-	-	+	+	-	-	-	NT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PG1exon3b6	+	+	+	+	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon3b7	+	-	+	+	-	+	+	NT	-	+	-	+	-	-	-	-	-	-	-	-	+	+	-	+	-	-	-	-	-	-
PG1exon3b8	-	-	-	-	-	-	-	NT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PG1exon5b6	+	+	-	-	-	-	+	NT	-	+	-	+	-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	-	-	-
PG1exon5b7	+	-	+	+	+	+	+	NT	+	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-
PG1exon5b8	-	-	-	+	-	-	-	NT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PG1exon56b	+	+	+	+	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon46b	+	+	+	+	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon36b	+	+	+	+	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon26b	+	+	+	+	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon16b	+	+	+	+	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+

[+] alternative splicing form with combination of exons 13478 instead of 1345678

FIG. 15

## ASSOCIATION STUDIES

POPULATIONS	AFFECTED N= [275;491]	UNAFFECTED N=[130;313]
	ALL CASES	CONTROLS
characteristics of populations	[275,491] all cases	<28 unaffected (65 years or older v & <289 controls (65 years or older v

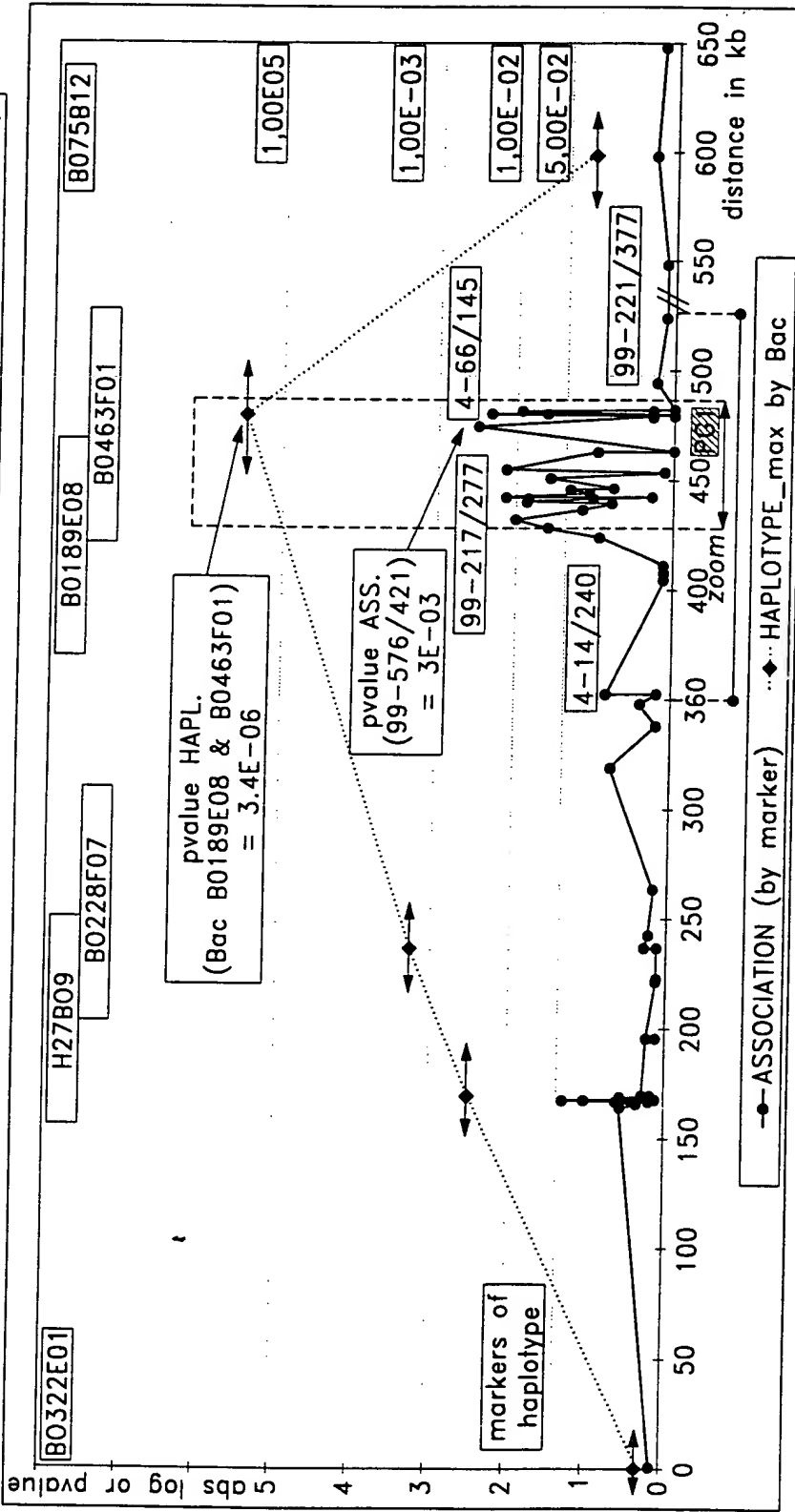
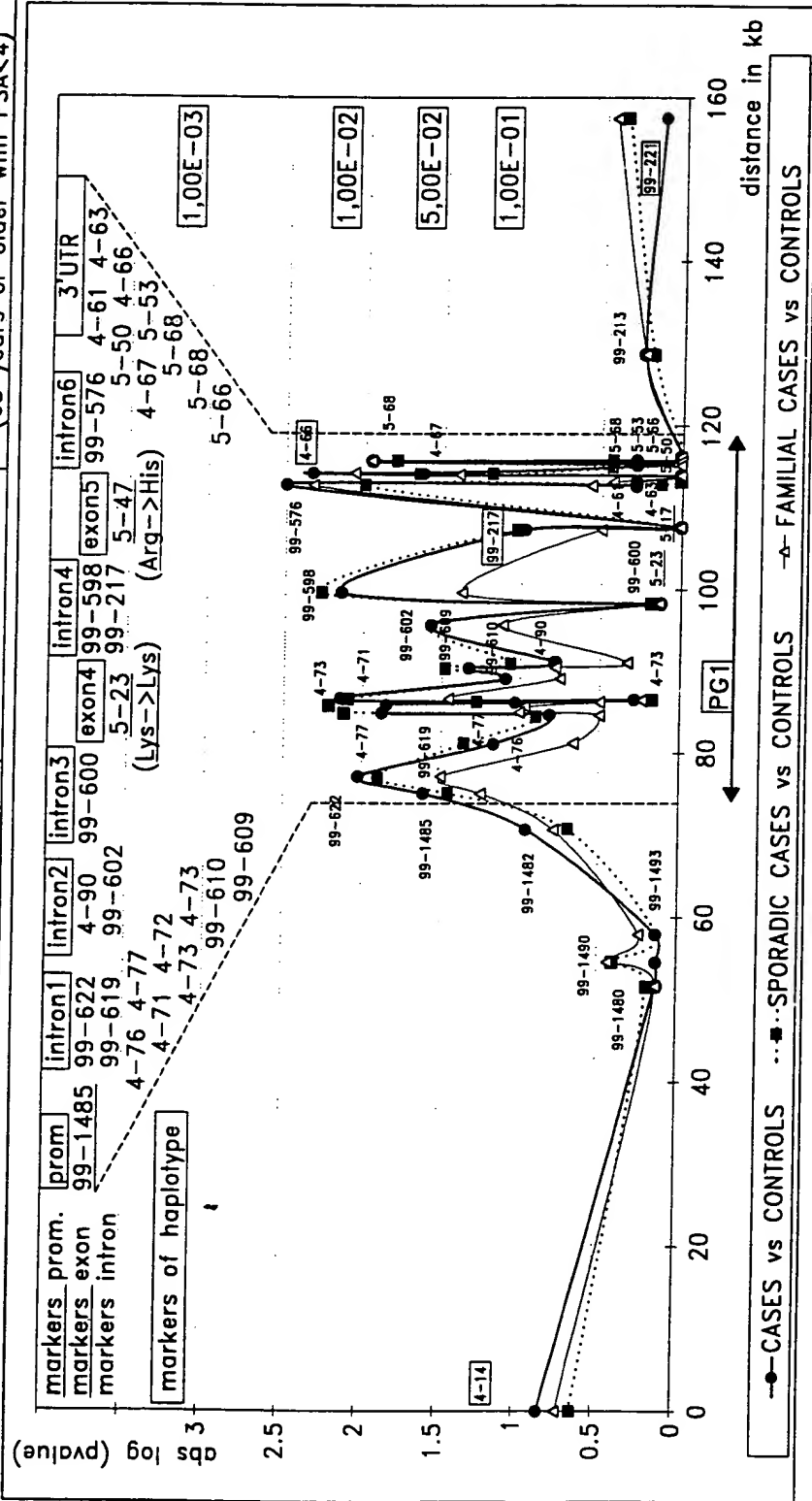


FIG. 17

## ASSOCIATION STUDIES

### PG1 (8p23)

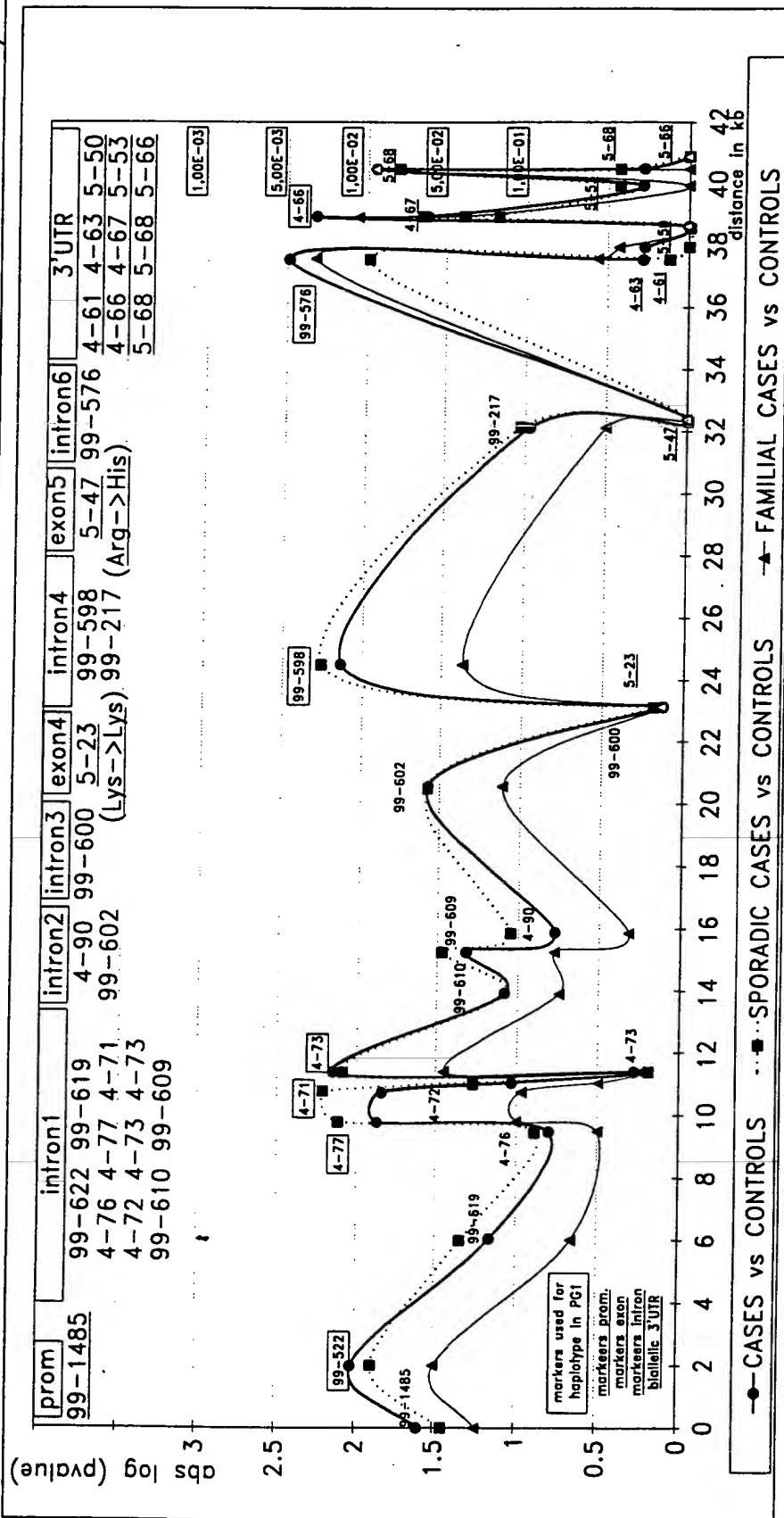
POPULATIONS	AFFECTED N= [275;491]			UNAFFECTED N=[130;313]
	ALL CASES	SPORADIC CASES	FAMILIAL CASES	CONTROLS
characteristics of populations	<=491 all cases	<=294 sporadics cases	<=197 familial cases	<28 unaffected (65 years or older) & <=289 controls (65 years or older with PSA<4)



## ASSOCIATION STUDIES

PG1 (8p23)

POPULATIONS	AFFECTED N= [275;491]			UNAFFECTED N=[130;313]
	ALL CASES	SPORADIC CASES	FAMILIAL CASES	
characteristics of populations	<=491 all cases	<=294 sporadics cases	<=197 familial cases	<28 unaffected (65 years or older) & <=289 controls (65 years or older with PSA<4)



name of markers	PG1	Polym.	Freq(cas)	Freq(controls)	abs diff % (fq(cases)- fq(controls))	Odd Ratio	Pvalue	Freq(randoms)	Attributable Risk
99-1485/251	prom	G*/T	0.32	0.24	7.4	1.44	2.53E-02	0.29	17.58
99-622/95	in1	G/T	0.52	0.42	10.1	1.51	9.64E-03	ND§	ND
99-619/141	in1	C/T	0.28	0.22	5.8	1.37	6.93E-02	ND	ND
4-76/222	in1	G/A	0.43	0.38	5	1.23	1.57E-01	0.41	13.15
4-77/151	in1	G/C	0.34	0.26	7.4	1.43	1.35E-02	0.31	18.16
4-71/233	in1	A/G	0.34	0.26	8.3	1.49	1.43E-02	0.28	18.64
4-72/127	in1	A/G	0.36	0.30	5.7	1.29	9.43E-02	0.31	13.25
4-73/134	in1	G/C	0.52	0.42	9.7	1.48	7.29E-03	0.52	26.76
99-610/250	in1	G/A	0.43	0.37	6.2	1.30	8.33E-02	ND	ND
99-609/225	in1	A/T	0.37	0.30	7	1.36	4.83E-02	ND	ND
4-90/283	in2	A/C	0.29	0.25	4.4	1.25	1.68E-01	0.28	9.32
99-602/258	in2	A/G	0.33	0.25	7.4	1.44	2.69E-02	ND	ND
99-600/492	in3	T/A	0.34	0.34	0.3	1.01	7.52E-01	ND	ND
99-598/130	in4	G/A	0.35	0.25	9.2	1.55	7.29E-03	ND	ND
99-217/277	in4	T/C	0.31	0.28	3.8	1.20	1.07E-01	0.28	8.46
99-576/421	in6	G/C	0.27	0.17	9.2	1.72	3.18E-03	0.24	18.40
4-61/269	3'UTR	G/A	0.01	0.00	0.3	1.76	0.527§	ND	ND
4-66/145	3'UTR	C/T	0.25	0.19	6.2	1.43	4.68E-03	0.24	13.16
4-67/40	3'UTR	T/C	0.25	0.20	4.9	1.33	2.39E-02	0.24	10.97

§ Test Fisher-§ ND: Not done -\* disease associated allele / not associated allele

FIG. 18B

## HAPLOTYPE FREQUENCY ANALYSIS

POPULATIONS	AFFECTED	UNAFFECTED
sample sizes	CASES (n=491)	CONTROLS (n=317)
characteristics of populations	294 sporadic cases + 197 familial cases	28 unaffected (65 years or older) + 289 controls (65 years or older with PSA<4)

PG1 (8p23)			4-14/240	99-217/277	4-66/145	99-221/377
distance between mks				in4	3'UTR	
size (cases vs controls)			<100kb>	<17kb>	<43kb>	
frequency % (cases/controls)			481vs305	481vs302	481vs300	481vs303
abs diff freq. all.(cases-controls)			65,7/62,1(C)	31,3/27,5(C)	25,1/19(C)	42,7/42,91 (A)
pvalue			3.6	3.8	6.2	0
Hardy Weinberg Disequilibrium			1.47E-01	1.07E-01	4.68E-03	7.52E-01
		cases	5.84E-01	6.55E-01	2.54E-01	5.84E-01
		controls	4.80E-01	2.21E-01	3.71E-01	2.54E-01
HAP 1 <43kb>	PT2	451 vs 297	<div style="display: flex; justify-content: space-between;"> <span>C</span> <span>T</span> <span>C</span> <span>A</span> </div>			
HAP 2 <17kb>		451 vs 296				
HAP 3 <117kb>		452 vs 299				
HAP 4 <100kb>		479 vs 302	C	T	C	
HAP 5 <60kb>		476 vs 300		T		A
HAP 6 <160kb>		476 vs 303	C			C
HAP 7 <160kb>	PT3	447 vs 297	C		C	A
HAP 8 <60kb>		446 vs 294		T	C	A
HAP 9 <117kb>		450 vs 296	C	T	C	
HAP 10 <160kb>		474 vs 300	C	T		A
HAP 11 <160kb>		445 vs 294	C	T	C	A

haplotype frequencies		Odd ratio	Chi-S	Pvalue	
cases	controls				
0.116	0.067	1.83	9.85	(1.7e-03)	***
0.243	0.183	1.43	7.49	(6.2e-03)	**
0.182	0.130	1.49	7.18	(7.3e-03)	**
0.217	0.188	1.20	1.88	(1.7e-01)	*
0.155	0.132	1.20	1.54	(2.1e-01)	*
0.373	0.346	1.12	1.16	(2.7e-01)	*
0.095	0.042	2.39	14.62	(1.3e-04)	****
0.117	0.065	1.93	11.33	(7.3e-04)	***
0.178	0.125	1.53	7.80	(5.2e-03)	**
0.114	0.089	1.32	2.44	(1.1e-01)	*
0.095	0.032	3.18	21.59	(3.4e-06)	*****

# FIG. 19B HAPLOTYPE FREQUENCY ANALYSIS PG1 (8p23)

markers of haplotype Max	4-14/240		99-217/277		4-66/145		99-221/377
			in4		3'UTR		
distance between mks	C		T		C		A
	<100kb>		<17kb>		<43kb>		

PG1	sample sizes	haplotype frequencies		odd ratio	chl-S	P value
		cases vs control	controls			
cases vs control	cases vs control	cases	controls			
cases (<=65 years) vs controls	455 vs 294	0.095	0.032	3.18	21.59	3.40E-06 *****
cases (>65 years) vs control	171 vs 294	0.105	0.032	3.56	20.91	4.60E-06 *****
sporadic cases vs controls	271 vs 294	0.079	0.032	2.60	12.13	4.80E-04 ****
sporadic cases (<=65 years) vs controls	266 vs 294	0.096	0.032	3.23	19.73	8.60E-06 *****
sporadic cases (>65 years) vs controls	85 vs 294	0.095	0.032	3.20	12.04	5.00E-04 ****
informative sporadic cases vs controls	178 vs 294	0.085	0.032	2.82	12.75	3.50E-04 ****
familial cases vs controls	67 vs 294	0.062	0.032	2.00	2.70	9.40E-02 **
familial cases (<=65 years) vs controls	179 vs 294	0.098	0.032	3.32	18.33	1.80E-05 *****
familial cases (>65 years) vs controls	86 vs 294	0.112	0.032	3.83	17.98	2.20E-05 *****
familial cases (>=3 caP) vs controls	93 vs 294	0.075	0.032	2.48	6.59	1.00E-02 **
	79 vs 294	0.123	0.032	4.26	21.33	3.70E-06 *****



## HAPLOTYPE FREQUENCY ANALYSIS (PG1)

Markers in PG1							
	size (cases vs controls)						
	allelic frequency % (cases / controls)						
	allelic frequency % (randoms)						
	diff freq. all. % (cases-controls)						
	pvalue (cases vs controls)						
	Odd Ratio						
	Attributable Risk %						
Hardy Weinberg Disequilibrium	cases						
	controls						
haplotype 1	2 MKS	339 vs 167					
haplotype 2	3 MKS	330 vs 122					
haplotype 3	4 MKS	312 vs 122					
haplotype 4	5 MKS	311 vs 121					
haplotype 5	6 MKS	309 vs 121					
haplotype 6	7 MKS	290 vs 99					

ND: Not Done

Comparison of Pvalue between nb of mks for haplotype  
(19 mks of PG1)

GENE	# of markers	# of 2 mks combinations	# of 3 mks combinations	# of mks combinations
PG1	19	171	969	3876

CUMULATIVE FREQUENCY HISTOGRAM OF Chi-square statistics (Chi-S) for PG1

